of the sequence of interest. In a cocktail of enzymes and substrates that includes a

second primer, reverse transcriptase, RNase H, RNA polymerase and ribo-and

deoxyribonucleoside triphosphates, the target sequence undergoes repeated rounds of

transcription, cDNA synthesis and second-strand synthesis to amplify the area of

5   interest. The use of 3SR to detect mutations is kinetically limited to screening small

segments of DNA (*e.g.*, 200-300 base pairs).

Q-Beta (Qβ) Replicase

In this method, a probe which recognizes the sequence of interest is attached to

the replicatable RNA template for Qβ replicase. A previously identified major

10   problem with false positives resulting from the replication of unhybridized probes has

been addressed through use of a sequence-specific ligation step. However, available

thermostable DNA ligases are not effective on this RNA substrate, so the ligation must

be performed by T4 DNA ligase at low temperatures (37°C). This prevents the use of

high temperature as a means of achieving specificity as in the LCR, the ligation event

15   can be used to detect a mutation at the junction site, but not elsewhere.

Table 1 below, lists some of the features desirable for systems useful in

sensitive nucleic acid diagnostics, and summarizes the abilities of each of the major

amplification methods (*See also*, Landgren, Trends in Genetics 9:199 [1993]).

A successful diagnostic method must be very specific. A straight-forward

20   method of controlling the specificity of nucleic acid hybridization is by controlling the

temperature of the reaction. While the 3SR/NASBA, and Qβ systems are all able to

generate a large quantity of signal, one or more of the enzymes involved in each

cannot be used at high temperature (*i.e.*, >55°C). Therefore the reaction temperatures

cannot be raised to prevent non-specific hybridization of the probes. If probes are

25   shortened in order to make them melt more easily at low temperatures, the likelihood

of having more than one perfect match in a complex genome increases. For these

reasons, PCR and LCR currently dominate the research field in detection technologies.

TABLE 1

FEATURE	METHOD:				
	PCR	LCR	PCR & LCR	3SR NASBA	Qβ
Amplifies Target	+	+	+	+	
Recognition of Independent Sequences Required	+	+	+	+	+
Performed at High Temp.	+	+			
Operates at Fixed Temp.				+	+
Exponential Amplification	+	+	+	+	+
Generic Signal Generation					+
Easily Automatable					

The basis of the amplification procedure in the PCR and LCR is the fact that the products of one cycle become usable templates in all subsequent cycles, consequently doubling the population with each cycle. The final yield of any such doubling system can be expressed as: $(1+X)^n = y$, where "X" is the mean efficiency (percent copied in each cycle), "n" is the number of cycles, and "y" is the overall efficiency, or yield of the reaction (Mullis, PCR Methods Applic., 1:1 [1991]). If every copy of a target DNA is utilized as a template in every cycle of a polymerase chain reaction, then the mean efficiency is 100%. If 20 cycles of PCR are performed, then the yield will be 2^{20}, or 1,048,576 copies of the starting material. If the reaction conditions reduce the mean efficiency to 85%, then the yield in those 20 cycles will be only 1.85^{20}, or 220,513 copies of the starting material. In other words, a PCR running at 85% efficiency will yield only 21% as much final product, compared to a reaction running at 100% efficiency. A reaction that is reduced to 50% mean efficiency will yield less than 1% of the possible product.

In practice, routine polymerase chain reactions rarely achieve the theoretical maximum yield, and PCRs are usually run for more than 20 cycles to compensate for the lower yield. At 50% mean efficiency, it would take 34 cycles to achieve the million-fold amplification theoretically possible in 20, and at lower efficiencies, the

number of cycles required becomes prohibitive. In addition, any background products that amplify with a better mean efficiency than the intended target will become the dominant products.

Also, many variables can influence the mean efficiency of PCR, including target DNA length and secondary structure, primer length and design, primer and dNTP concentrations, and buffer composition, to name but a few. Contamination of the reaction with exogenous DNA (*e.g.*, DNA spilled onto lab surfaces) or cross-contamination is also a major consideration. Reaction conditions must be carefully optimized for each different primer pair and target sequence, and the process can take days, even for an experienced investigator. The laboriousness of this process, including numerous technical considerations and other factors, presents a significant drawback to using PCR in the clinical setting. Indeed, PCR has yet to penetrate the clinical market in a significant way. The same concerns arise with LCR, as LCR must also be optimized to use different oligonucleotide sequences for each target sequence. In addition, both methods require expensive equipment, capable of precise temperature cycling.

Many applications of nucleic acid detection technologies, such as in studies of allelic variation, involve not only detection of a specific sequence in a complex background, but also the discrimination between sequences with few, or single, nucleotide differences. One method for the detection of allele-specific variants by PCR is based upon the fact that it is difficult for *Taq* polymerase to synthesize a DNA strand when there is a mismatch between the template strand and the 3' end of the primer. An allele-specific variant may be detected by the use of a primer that is perfectly matched with only one of the possible alleles; the mismatch to the other allele acts to prevent the extension of the primer, thereby preventing the amplification of that sequence. This method has a substantial limitation in that the base composition of the mismatch influences the ability to prevent extension across the mismatch, and certain mismatches do not prevent extension or have only a minimal effect (Kwok *et al.*, Nucl. Acids Res., 18:999 [1990]).)